*EXHIBIT Q*

## ☒ NCBI   **Blast 2 Sequences results**

| PubMed | Entrez | BLAST | OMIM | Taxonomy | Structure |
|--------|--------|-------|------|----------|-----------|

## BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.2 [Dec-14-2001]

Match: `1`   Mismatch: `-2`   gap open: `5`   gap extension: `2`

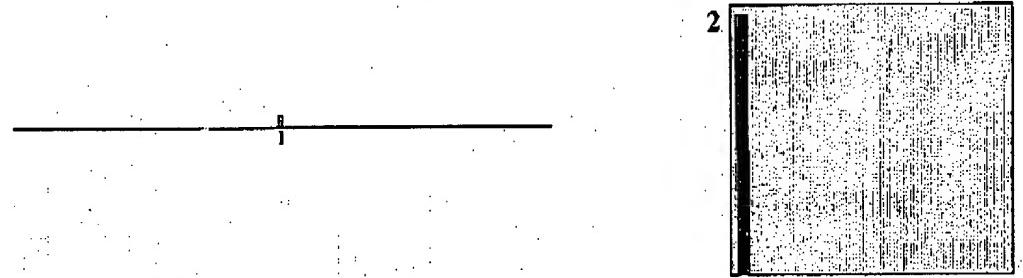x_dropoff: `50`   expect: `10.000`   wordsize: `11`   Filter ☑   [ Align ]

**Sequence 1**   gi 1302.7635   Homo sapiens endothelial differentiation, sphingolipid G-protein-coupled receptor, 1 (EDG1), mRNA   **Length** 2753   (1 .. 2753)

**Sequence 2**   lcl|seq_2                                                      **Length** 25   (1 .. 25)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence

```
Score = 43.0 bits (22), Expect = 1.6
Identities = 24/25 (96%)
 Strand = Plus / Minus
```

```
Query: 118  ctacacaaaaagcctggatcactca 142
            ||||||||||||| |||||||||||
Sbjct: 25   ctacacaaaaagcttggatcactca 1
```

```
CPU time:    0.06 user secs.       0.05 sys. secs      0.11 total secs.

Lambda    K       H
  1.33    0.621    1.12

Gapped
Lambda    K       H
  1.33    0.621    1.12


Matrix: blast matrix:1 -2
Gap Penalties: Existence: 5, Extension: 2
Number of Hits to DB: 1
```

```
Number of Sequences: 0
Number of extensions: 1
Number of successful extensions: 1
Number of sequences better than 10.0: 1
length of query: 2753
length of database: 5,006,917,935
effective HSP length: 25
effective length of query: 2728
effective length of database: 5,000,452,710
effective search space: 13641234992880
effective search space used: 13641234992880
T: 0
A: 30
X1: 6 (11.5 bits)
X2: 26 (50.0 bits)
S1: 12 (23.8 bits)
S2: 21 (41.1 bits)
```